Mailed

OIPE JC66 3rd Floor
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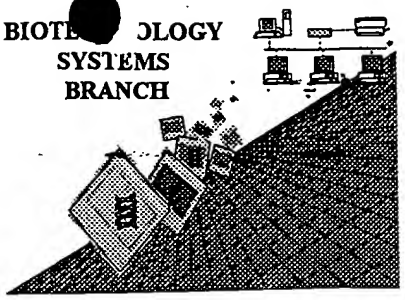
#7

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/367,013A

Source: 1652

Date Processed by STIC: 7/31/2000

RECEIVED
FEB 22 2001
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

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1652

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A TIME: 16:10:58

Input Set : A:\Cgab1.app
Output Set: N:\CRF3\08012000\I367013A.raw

3 <110> APPLICANT: KNUTZON, DEBORAH
4 MUKERJI, PRADIP
5 HUANG, YUNG-SHENG
6 THURMOND, JENNIFER
7 CHAUDHARY, SUNITA
8 LEONARD, AMANDA E.
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN
11 POLYUNSATURATED FATTY ACIDS
13 <130> FILE REFERENCE: CGAB-210 USA
15 <140> CURRENT APPLICATION NUMBER: 09/367,013A
16 <141> CURRENT FILING DATE: 1999-08-05
18 <150> PRIOR APPLICATION NUMBER: 08/834,655
19 <151> PRIOR FILING DATE: 1997-04-11
21 <160> NUMBER OF SEQ ID NOS: 40
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1617
27 <212> TYPE: DNA
28 <213> ORGANISM: Mortierella alpina
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
33 <400> SEQUENCE: 1
34 cgacactcct tccttcttct cacc
35 acaacaaacc atggctgctg ctcc
36 tgccgaggct ctgaatgagg gcaa
37 caacaaggtg tacgatgtcc gcga
38 cacgcacgtt ggcaaggacg gcac
39 ggagactctt gccaactttt acgt
40 tgatgacttt gcggccgagg tccg
41 cgattcttcc aaggcatact acgc
42 gtcgacggtc attgtggcca agtg
43 tgcgcttttg ggtctgttct ggca
44 ccaggtcttc caggaccgtt tctg
45 ccagggcttc tcgtcctcgt ggtg
46 cgtccacggc gaggatcccg acatt
47 gttggagatg ttctcggatg tccca
48 ggtcctgaac cagacctggt tttac
49 cctccagtcc attctctttg tgctg
50 tgtgcccatc tcgttggtcg agcag
51 caccatgttc ctgttcatca aggat
52 ggcggtgtgc ggaaacttgt tggcg
53 gatctcgaag gaggaggcgg tcgat
54 tgatgtccac ccgggtctat ttgcc
55 gcaccacttg ttcccttcga tgcct
56 gaccctgtgc aaaaagtaca atgtc
57 agaggtcttt agccgtctga acgagg
58 gtaaaaaaaa aaacaaggac gttttt

Nucleotide Sequence

← No response shown. Response is mandatory when sequence is combined DNA/RNA.

See 1.823 f
New Sequence Rules

TC 1600 MAIL ROOM RECEIVED

RAW SEQUENCE LISTING DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

59 tgtcaagtcg agcgtttctg gaaaggatcg ttcagtgcag tatcatcatt ctccttttac 1560
60 cccccgctca tatctcattc atttctcttg ttaaacaact tgttcccccc ttcaccg 1617
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 457
65 <212> TYPE: PRT
66 <213> ORGANISM: Mortierella alpina
68 <400> SEQUENCE: 2
69 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
70 1 5 10 15
72 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
73 20 25 30
75 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
76 35 40 45
78 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
79 50 55 60
81 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
82 65 70 75 80
84 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 85 90 95
87 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
88 100 105 110
90 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
91 115 120 125
93 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
94 130 135 140
96 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
97 145 150 155 160
99 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
100 165 170 175
102 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
103 180 185 190
105 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
106 195 200 205
108 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
109 210 215 220
111 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
112 225 230 235 240
114 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
115 245 250 255
117 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
118 260 265 270
120 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
121 275 280 285
123 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
124 290 295 300
126 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
127 305 310 315 320
129 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
130 325 330 335

RAW SEQUENCE LISTING DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A TIME: 16:10:58

Input Set : A:\Cgab1.app
Output Set: N:\CRF3\08012000\I367013\.raw

```
132 Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His
133             340                 345                 350
135 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
136         355                 360                 365
138 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
139     370                 375                 380
141 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
142 385                 390                 395                 400
144 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
145                 405                 410                 415
147 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
148             420                 425                 430
150 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
151         435                 440                 445
153 Ala Ala Ser Lys Met Gly Lys Ala Gln
154     450                 455
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 1488
159 <212> TYPE: DNA
160 <213> ORGANISM: Mortierella alpina
162 <400> SEQUENCE: 3
163 gtcccctgtc gctgtcggca cacccatcc tccctcgctc cctctgcgtt tgtccttggc 60
164 ccaccgtctc tcctccaccc tccgagacga ctgcaactgt aatcaggaac cgacaaatac 120
165 acgatttctt tttactcagc accaactcaa aatcctcaac cgcaaccctt tttcaggatg 180
166 gcacctccca acactatcga tgccggtttg acccagcgtc atatcagcac ctcggcccca 240
167 aactcggcca agcctgcctt cgagcgcaac taccagctcc ccgagttcac catcaaggag 300
168 atccgagagt gcatccctgc ccactgcttt gagcgctccg gtctccgtgg tctctgccac 360
169 gttgccatcg atctgacttg ggcgtcgctc ttgttcctgg ctgcgaccca gatcgacaag 420
170 tttgagaatc ccttgatccg ctatttggcc tggcctgttt actggatcat gcagggtatt 480
171 gtctgcaccg gtgtctgggt gctggctcac gagtgtggtc atcagtcctt ctcgacctcc 540
172 aagaccctca acaacacagt tggttggatc ttgcactcga tgctcttggt cccctaccac 600
173 tcctggagaa tctcgcactc gaagcaccac aaggccactg gccatatgac caaggaccag 660
174 gtctttgtgc ccaagacccg ctcccaggtt ggcttgcctc ccaaggagaa cgctgctgct 720
175 gccgttcagg aggaggacat gtccgtgcac ctggatgagg aggctcccat tgtgactttg 780
176 ttctggatgg tgatccagtt cttgttcgga tggcccgcgt acctgattat gaacgcctct 840
177 ggccaagact acggccgctg gacctcgcac ttccacacgt actcgcccat ctttgagccc 900
178 cgcaactttt tcgacattat tatctcggac ctcggtgtgt tggctgccct cggtgccctg 960
179 atctatgcct ccatgcagtt gtcgctcttg accgtcacca agtactatat tgtcccctac 1020
180 ctctttgtca acttttggtt ggtcctgatc accttcttgc agcacaccga tcccaagctg 1080
181 ccccattacc gcgagggtgc ctggaatttc cagcgtggag ctctttgcac cgttgaccgc 1140
182 tcgtttggca agttcttgga ccatatgttc cacggcattg tccacaccca tgtggcccat 1200
183 cacttgttct cgcaaatgcc gttctaccat gctgaggaag ctacctatca tctcaagaaa 1260
184 ctgctgggag agtactatgt gtacgaccca tccccgatcg tcgttgcggt ctggaggtcg 1320
185 ttccgtgagt gccgattcgt ggaggatcag ggagacgtgg tctttttcaa gaagtaaaaa 1380
186 aaaagacaat ggaccacaca caaccttgtc tctacagacc tacgtatcat gtagccatac 1440
187 cacttcataa aagaacatga gctctagagg cgtgtcattc gcgcctcc              1488
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 399
192 <212> TYPE: PRT
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RAW SEQUENCE LISTING DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

<213> ORGANISM: Mortierella alpina
<400> SEQUENCE: 4

```
Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
 1               5                  10                  15
Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
            20                  25                  30
Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
        35                  40                  45
His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
    50                  55                  60
Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
65                  70                  75                  80
Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
                85                  90                  95
Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
            100                 105                 110
Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
        115                 120                 125
Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
    130                 135                 140
Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Th  Lys Asp
145                 150                 155                 160
Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
                165                 170                 175
Glu Asn Ala Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
            180                 185                 190
Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
        195                 200                 205
Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
    210                 215                 220
Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
225                 230                 235                 240
Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
                245                 250                 255
Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
            260                 265                 270
Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
        275                 280                 285
Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
    290                 295                 300
Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
305                 310                 315                 320
Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
                325                 330                 335
Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
            340                 345                 350
Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
        355                 360                 365
Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
```

RAW SEQUENCE LISTING DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

```
266     370                 375                 380
268 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
269 385                 390                 395
272 <210> SEQ ID NO: 5
273 <211> LENGTH: 355
274 <212> TYPE: PRT
275 <213> ORGANISM: Mortierella alpina
277 <400> SEQUENCE: 5
278 Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp
279   1               5                  10                  15
281 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
282              20                  25                  30
284 Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
285          35                  40                  45
287 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
288      50                  55                  60
290 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
291  65                  70                  75                  80
293 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
294                  85                  90                  95
296 Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
297             100                 105                 110
299 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
300         115                 120                 125
302 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
303     130                 135                 140
305 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
306 145                 150                 155                 160
308 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
309                 165                 170                 175
311 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
312             180                 185                 190
314 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
315         195                 200                 205
317 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
318     210                 215                 220
320 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
321 225                 230                 235                 240
323 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
324                 245                 250                 255
326 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
327             260                 265                 270
329 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
330         275                 280                 285
332 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
333     290                 295                 300
335 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
336 305                 310                 315                 320
338 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 08/01/2000
PATENT APPLICATION: US/09/367,013A TIME: 16:10:59

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

L:360 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:360 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:360 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:366 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:366 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:444 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:444 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:447 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:465 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:493 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:493 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:558 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:558 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:558 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:726 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:736 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:736 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
M:340 Repeated in SeqNo=21
L:744 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:757 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:757 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:757 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:760 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:760 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:1173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/367,013A

DATE: 08/01/2000
TIME: 16:10:59

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

L:1173 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:1176 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1176 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:1182 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1182 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1185 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1185 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
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L:1232 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1232 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
L:1235 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1235 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:1238 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1238 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1272 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:1330 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:1401 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1529 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:1684 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40

OIPE JC66
FEB 0 9 2001
PATENT & TRADEMARK OFFICE

Application No.: 09/367,013

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [ ] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- [ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] 7. Other: _

Applicant Must Provide:

- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
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